

a) producing a collection of DNA fragments encoding SH3 domains containing a randomized mutations in RT-loop (RRT-SH3 domains),

b) generating recombinant libraries comprising said RRT-SH3 domains,

c) subjecting said libraries to affinity or functional selection steps to identify artificial SH3 domains, and

d) selecting domains with an binding affinity that is higher than the binding affinity of the corresponding wild-type SH3 domain.

C²
17. (Twice Amended) The method according to claim 3, wherein the six amino acids that are replaced in the RT-loop are replaced with a peptide motif derived from Hck-SH3 and which binds to HIV-1 Nef protein selected from the group consisting of XSWSXX (SEQ ID NO:28), XSPFXX (SEQ ID NO:30) and XSXFPW (SEQ ID NO:32), wherein X is any amino acid.
